



01 13 06 SeqListg CEN0250NP.txt

<110> Giles-Komar, Jill; David Shealy; David Knight; Bernie Scallon; George Heavner

<120> ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES

<130> CEN0250 NP

<140> US 09/920,137

<141> 2001-08-01

<150> 60/223,360

<151> 2000-08-07

<150> 60/236,826

<151> 2000-09-29

<160> 35

<170> PatentIn Ver 3.1

<210> 1

<211> 5

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<213> Homo sapiens

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<222> (1)..(5)

<223> Heavy Chain complementarity determinng region 1 (CDR1).

<400> 1

Ser Tyr Ala Met His
1 5

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<211> 17

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<222> (1)..(17)

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<222> (1)..(1)

<223> Xaa at position 1 is selected from Ile, Phe or Val.

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> Xaa at position 2 is selected from Ile or Met.

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> Xaa at position 3 is selected from Ser or Leu.

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> Xaa at position 4 is selected from Tyr or Phe.

<220>

<221> MISC_FEATURE

<222> (10)..(10)

<223> Xaa at position 10 is selected from Lys or Tyr.

<220>

<221> MISC_FEATURE

<222> (11)..(11)

<223> Xaa at position 11 is selected from Ser or Tyr.

<220>

<221> MISC_FEATURE

<222> (17)..(17)

<223> Xaa at position 17 is selected from Asp or Gly.

<400> 2

| | | | | | | | | | | | | | | | | | |
|---|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | Xaa | Xaa | Xaa | Xaa | Asp | Gly | Ser | Asn | Lys | Xaa | Xaa | Ala | Asp | Ser | Val | Lys | Xaa |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | | |

<210> 3

<211> 17

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<213> Homo sapiens

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<221> MISC_FEATURE

<222> (1)..(17)

<223> Heavy Chain complementarity determinng region 3 (CDR3).

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> Xaa at position 4 is selected from Ile or Val.

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<222> (5)..(5)

<223> Xaa at position 5 is selected from Ser, Ala or Gly.

<220>

<221> MISC_FEATURE

<222> (9)..(9)

<223> Xaa at position 9 is selected from Asn or Tyr.

<400> 3

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Arg | Gly | Xaa | Xaa | Ala | Gly | Gly | Xaa | Tyr | Tyr | Tyr | Tyr | Gly | Met | Asp | Val |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |

<210> 4

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 <223> Light Chain complementarity determinng region 1 (CDR1).

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 <222> (7)..(7)
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 Arg Ala Ser Gln Ser Val Xaa Ser Tyr Leu Ala
 1 5 10

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 <223> Light Chain complementarity determinng region 2 (CDR2).

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 <211> 10
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 <223> Light Chain complementarity determinng region 3 (CDR3).

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 1 5 10

<210> 7
 <211> 126
 <212> PRT
 <213> Homo sapiens
 <400> 7

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr
 20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Asn Gly Leu Glu Trp Val
 35 40 45

Ala Phe Met Ser Tyr Asp Gly Ser Asn Lys Lys Tyr Ala Asp Ser Val
 Page 3

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Arg Gly Ile Ala Ala Gly Gly Asn Tyr Tyr Tyr Tyr Gly
 100 105 110
 Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 8
 <211> 108
 <212> PRT
 <213> Homo sapiens
 <400> 8

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Tyr Ser Tyr
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45
 Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80
 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
 85 90 95
 Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
 100 105

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 <222> (1)..(157)
 <223> human TNF alpha monomer sequence

<400> 9

Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val
 1 5 10 15
 Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
 20 25 30
 Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
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35

val val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
50 55 60
Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
65 70 75 80
Ser Arg ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
85 90 95
Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
100 105 110
Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys
115 120 125
Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
130 135 140
Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
145 150 155

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<400> 10
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18

<210> 11
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<400> 11
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<211> 30
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<400> 12
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gccgcacgtg tggaaggg

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<210> 14
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<400> 14
 agtcaaggctc ggactggctt aagtt 25

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<400> 15
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<400> 16
 ggcggtagac tactcgtc 18

<210> 17
 <211> 7
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<400> 17
 Met Asp Trp Thr Trp Ser Ile
 1 5

<210> 18
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<400> 18
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<400> 19
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 <212> DNA
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<400> 20
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tttcgtacgc caccatgaaa cacctgtggt tcttc 35

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<400> 22

tttcgtacgc caccatgggg tcaaccgcca tcctc 35

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Thr val Thr val Ser Ser
1 5

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<400> 24

gtgccagtgg cagaggagtc cattcaagct taagtt 36

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<400> 25

Met Asp Met Arg val
1 5

<210> 26
<211> 31
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<400> 26

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<211> 28
<212> DNA
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<400> 27

tttgctgaca ccatggaagc cccagctc 28

<210> 28
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 <213> Homo sapiens

<400> 28

Thr Lys Val Asp Ile Lys
 1 5

<210> 29
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<400> 29

ctggtttcac ctatagtttg cattcagaat tcggcgcctt t 41

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<400> 31

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 <222> (1)..(19)
 <223> Signal sequence for heavy chain variable region sequences as presented in original

Figure 4

<400> 32

Met Gly Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg Gly
 1 5 10 15

Val Gln Cys

<210> 33
 <211> 20
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<222> (1)..(20)

<223> Signal sequence for light chain variable region sequences as presented in original

Figure 5

<400> 33

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15
Asp Thr Thr Gly
20

<210> 34

<211> 428

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(421)

<223> heavy chain variable region DNA sequences as presented in original Figure 2A-2B

<400> 34

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gtgcagctgg tggagtctgg gggaggcgtg gtccagcctg ggaggtccct gagactctcc 120
tgtgcagcct ctggttcacc ttcagtagct atgctatgca ctgggtccgc caggctccgg 180
caaggggctg gagtgggtgg cagttatatc atatgatgga aaataaatac tacgcagact 240
ccgtgaaggg ccgattcacc atctagagac aattccaaga acacgctgta tctgcaaata 300
aacagccaga gctgaggaca cggctgtgta ttactgtgcg agagatcgag gtatatcagc 360
aggtggaata ctactactac tacggtatgg acgtctgggg gcaagggacc acggtcaccg 420
tctcctca 428
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<210> 35

<211> 387

<212> DNA

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<220>

<221> CDS

<222> (1)..(387)

<223> light chain variable region DNA sequences as presented in original Figure 3

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gaaatttgtt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 120
ctctcctgca gggccagtca gagtggttag agctacttag cctggtagca acagaaacct 180
ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 240
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 300
gaagattttg cagtttatta ctgtcagcag cgtagcaact ggcctccatt cactttcggc 360
cctgggacca aagtggatat caaacgt 387
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